

Figure 1A

1	GAGACAAAATTTGAGGGTGGGATCCACTGAGGAGTACATAGACTGCTGGATTCTGGTGG	60
61	AGCCAGACACTGGTCCCAACGGGTGGTATCTGGCTCCTGTGGAGGGGGGTACGTGAGGGG	120
121	GGGGGTACTGGGGCTTATTCTCAGGTACCTGTGGGTGGGATCAGCGAGGGTACCTGAGCG	180
181	TCAAGAGCATACCCTAGTGAGCGGGCTCCTCTGGGGGAGACCAGCGCGCTCCGGGCGCCT	240
241	GCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGGCGGCGCTGGCCAGTAGCCTGATCC	300
1	<u>M A A L A S S L I R</u>	10
301	GGCAGAAGCGGGAGGTCCGCGAGCCCGGGGCGAGCCGGCCGGTGTGCGGCGCAGCGGCGCG	360
11	<u>Q K R E V R E P G G S R P V S A Q R R V</u>	30
361	TGTGTCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGG	420
31	C P R G T K S L C Q K Q L L I L L S K V	50
421	TGCGACTGTGCGGGGGCGGCCCCGCGCGGCGGACCGCGGCGGAGCCTCAGCTCAAAG	480
51	R L C G G R P A R P D R G P E P Q L K G	70
481	GCATCGTCACCAAACTGTTCTGCGCGCAGGGTTTCTACCTCCAGGCGAATCCCGACGGAA	540
71	I V T K L F C R Q G F Y L Q A N P D G S	90
541	GCATCCAGGGCACCCAGAGGATACCAGCTCCTTCAACCACTTCAACCTGATCCCTGTGG	600
91	I Q G T P E D T S S F T H F N L I P V G	110
601	GCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTG	660
111	L R V V T I Q S A K L G H Y M A M N A E	130
661	AGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCGCTTTAAGGAGTGTGTCT	720
131	G L L Y S S P H F T A E C R F K E C V F	150
721	TTGAGAATTACTACGTCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGG	780
151	E N Y Y V L Y A S A L Y R Q R R S G R A	170
781	CCTGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCAATGAAGGAAACCGAGTTAAGAAGA	840
171	W Y L G L D K E G Q V M K G N R V K K T	190
841	CCAAGGCAGCTGCCCCACTTTCTGCCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTT	900
191	K A A A H F L P K L L E V A M Y Q E P S	210
901	CTCTCCACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCCTGAAATGTAGTCC	960
211	L H S V P E A S P S S P P A P *	226
961	CTGGACTGGAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGTCTCCAG	1020

**Figure 1B**

1021 TCCTGCTCTCACCCTGCTGCCACACACATGCCCTGAGCAGCCAGGTCCCCTAGGTGCT 1080  
1081 CTACCCTGAGGGAGCCTAGGGGCTGACTGTGACTTCCGAGGGTGCTGAGCACCTTAGAT 1140  
1141 CTTTGGGCCTAGGAGGGAGTCAGAGAGGGGGATGTCTGAAGATGGTCCTGGCTGATCACT 1200  
1201 TCTTTCCTTCCACACTCACACAACCCCATGTCCTTTTCCTGAGATGGCGCTGGGAGTTCC 1260  
1261 CACATGGACAGCCAGGGCATAAACACTTCCCACCCCGGATCAGACAGTTCCCTGGAG 1317

### Figure 2

		10		20		30		40																																			
1		M	A	P	L	G	E	-	-	V	G	N	Y	F	G	V	Q	D	A	V	P	F	G	N	V	P	V	L	P	V	D	S	P	V	-	-	-	-	-	-	FGF-9.aa		
1		M	A	A	L	A	S	S	L	T	R	O	K	R	E	V	R	E	F	-	-	-	-	G	G	S	R	P	V	S	A	Q	R	R	V	C	P	R	G	T	K	S	FGF-14.aa
		50		60		70		80																																			
32		-	-	-	-	-	-	L	L	S	D	-	H	L	G	Q	S	E	A	G	G	I	P	R	G	P	A	V	T	D	L	D	H	L	K	G	I	I	R	FGF-9.aa			
38		L	C	Q	K	Q	L	L	I	L	L	S	K	V	R	L	C	G	G	R	E	A	R	E	D	R	G	P	E	-	-	-	-	Q	L	K	G	I	V	T	FGF-14.aa		
		90		100		110		120																																			
63		R	R	Q	L	Y	C	R	T	G	F	H	L	E	I	F	P	N	G	T	I	Q	G	T	R	K	D	H	S	R	F	G	I	L	E	F	I	S	I	A	V	FGF-9.aa	
74		K	-	-	L	F	C	R	O	G	F	Y	L	Q	A	N	P	D	G	S	I	Q	G	T	P	E	D	T	S	S	F	T	H	E	N	L	I	P	V	G	L	FGF-14.aa	
		130		140		150		160																																			
103		G	L	V	S	I	R	G	V	D	S	G	L	Y	L	G	M	N	E	K	G	E	L	Y	G	S	E	K	L	T	Q	E	C	V	F	R	E	-	Q	F	E	FGF-9.aa	
112		R	V	V	T	I	Q	S	A	K	L	G	H	Y	M	A	M	N	A	E	G	L	L	Y	S	S	P	H	E	T	A	E	C	R	F	K	E	C	V	F	E	FGF-14.aa	
		170		180		190		200																																			
142		E	N	W	Y	N	T	Y	S	S	N	L	Y	K	H	V	D	T	G	R	R	Y	Y	V	A	L	N	K	D	G	T	P	R	E	G	T	R	T	K	R	H	FGF-9.aa	
152		N	Y	-	Y	V	L	Y	A	S	A	L	Y	R	Q	R	R	S	G	R	A	W	Y	I	G	L	D	K	E	G	O	V	M	K	G	N	R	V	K	K	T	FGF-14.aa	
		210		220		230																																					
182		Q	K	F	T	H	F	L	P	R	P	V	D	F	D	-	-	-	-	-	-	-	-	K	V	P	E	L	Y	K	D	I	L	S	Q	S					FGF-9.aa		
191		K	A	A	A	H	F	L	P	K	L	L	E	V	A	M	Y	Q	E	P	S	L	H	S	V	P	E	A	S	P	S	S	P	P	A	P	.					FGF-14.aa	

Figure 3

